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Motif 0
AKFLHMLMSVVVELLRSSFFVYVTFQKNR
ISEIEMVLGKRSNAKMCLSDFEKRRQIFAETIWLNSFIPIILQSSFFYTSSDLRNR
LKDFRWLFISD---IWFTHNPNLNQLAICFISWLFRLPKIIQTFFCYCTEISSVT-
TREISWMQVET-SAKHFYYFDHEN-IYVLWKLRLRWIFEDLVSLIRCFYVTEQQKSYSK
* *** **

human
tez1
EST2
p123

Motif 1
LFFYRKSVWSKLQSIGIRQHLKRVQRDVSEAEVRQHREARPALTSRLRFIPKP--DGL
TVYFRKDIWKLRCRPFITSMKMEAFKINENNVNMDTQK-TTLPNAVIRLLPKK--NTF
IVYFRHDTWKNLITPFIIVEYFKTYLVENNVCRNHSYTLS--NFNHSKMRIIPKKSNEF
TYVYRKNIWDVIMKMSI-ADLKKETLAEVQKEVEEMWKS-LGFAPGKRLRLIPKK--TTF
* * *

human
tez1
EST2
p123

Motif 2
RPIVNM DYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
RLITN-LRKRFLIKMGSKKMLVSTNQTLRPVASILKHLINCESSGIPFNLEVYMKLLTF
RIIAIPCRGADEEFTIYKENHKNAIQPTQKILEYLRNKRPTSTFKIYSPTQIADRIKEF
RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGFVFNVDVMMKKY
* * *

human
tez1
EST2
p123

Motif 3 (A)
KKDLLKHRMFGFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
KQRLKKFNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
* * * * *

tez1
EST2
p123

FIG. 1

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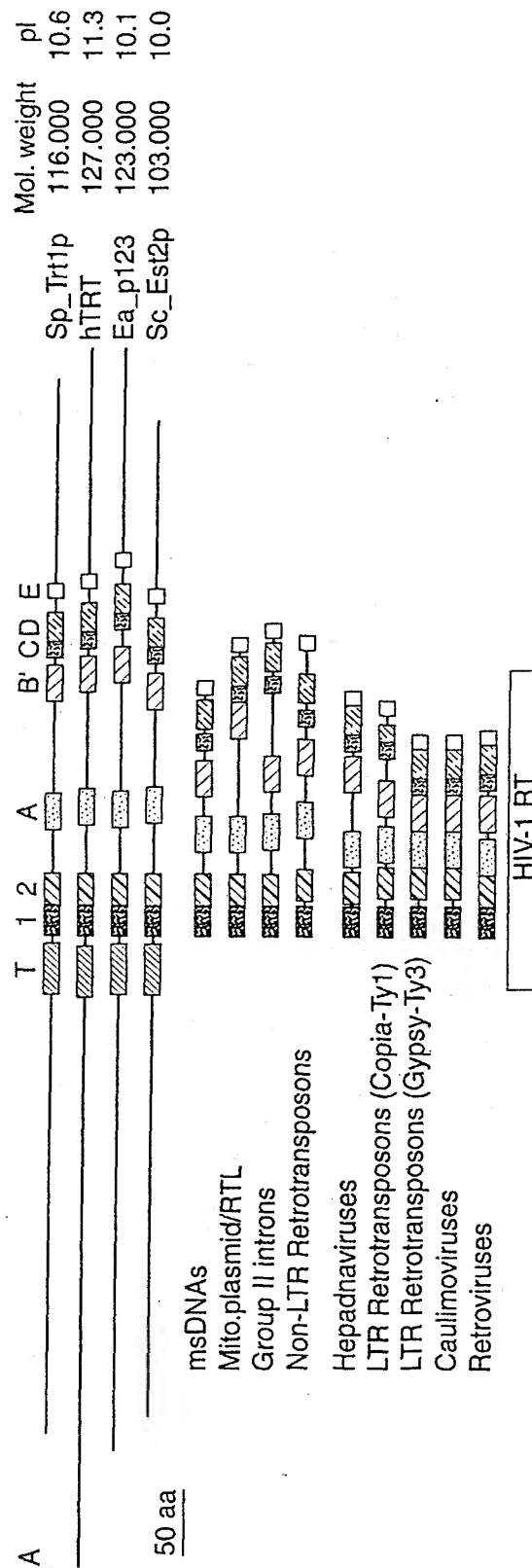


FIG. 2

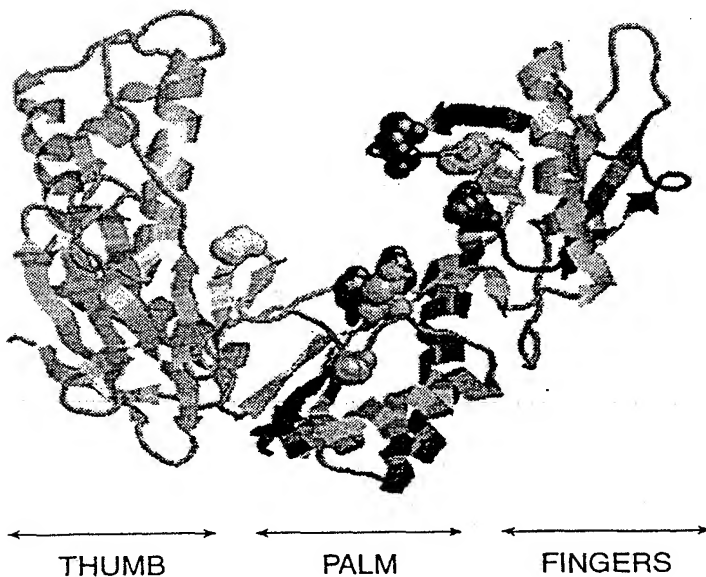


FIG. 3

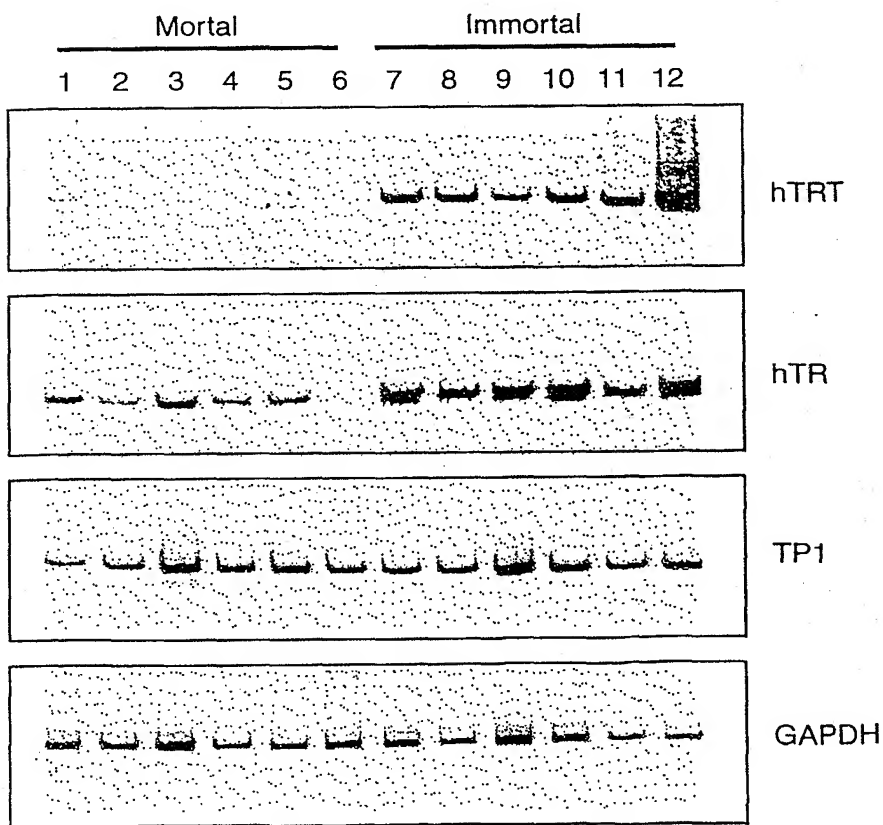


FIG. 5

Motif T		Motif 1		Motif 2		Motif A	
TRT con	WL	hh hh pFFY TE p	p	Y RK W L h I K		PcLYFh hDh CYD I	hhk K
Sp_Trt1p	429	WLYNSFIPILOSFYITESSDLNRVTYFRKDIWKLRCRPFITSMKM	8				
hTRT	546	WLMVSVVVELLSFFVVTETTFQKNRLLFFRKSVMSKLSQSIGIRQHLK	10				
Ea_p123	441	WIFEDLVSLIRCFYVTEQQKSYSKTYVYRNINWDVIMKMSIADLKK	8				
Sc_Est2p	366	WLFRLQILPKIIQTFYCTEISSTVT-IVYFRHDTWNKLITPFIVEYFK	8				
Motif B'		Motif C		Motif D		Motif E	
TRT con	K Y Q	GIPQGS LS hL h Y DL	F	LLRL DDFlhIT	A F h G c p N cK	W G S	
Sp_Trt1p	SOYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFT	6	LLRVDDFLFITVNNKD	0	AKKFLNLSLRGFEKHNFTSLEKTVI	17	KKRMPPFFGSV 181
hTRT	KSYVQCQIPQGSILSTLLCSLCYGDMMENKLFAGI	5	LLRLVDDFLVTPHLTH	0	AKTFLRTLVRGVPEYGCVVNLRKTVV	19	HGLFPWCGLLL 197
Ea_p123	KFYKQTKGIPQGLCVSSILSSFYATLEESSLGFL	14	LMRLTDDVLLITTOENN	0	AVLFIEKLINVSRENGFKFNMKLQOT	23	QDYCDWIGISI 179
Sc_Est2p	KCYIREDGLEQGSLSAPIVDLVYDDLLLEFYSEFK	8	ILKLADDFLLIISTDQQQ	0	VINIKKLAMGGFQKYNKAKANRDKILA	20	KELEVWKSST 146
Motif B		Motif C		Motif D		Motif E	
RT con	hPQG	pp hh h	h Y Dhhhh	Gh h cK h	hLG h		
Sc_a1	TYHKPMLGLPQGSILSPILCNIVMTLVDNWLEDYI	55	YVRVADDILIGVLGSKN	2	KMIKRDNLNNFLNS-LGLTMNEEKTLI	4	ETPARFLGYNI
Dm_TART	RAGQIGAGVPQGSNLGPILYSIFSSDMPLPHIYHP	7	LSTYADDTIVLSSDILA	6	NENYLKTFSDWADKWGISVNAAKTGH	25	ESKQSYLGVIL
HIV-1	GIRYQYNVLPQGNKGSIPAIFQSSMTKILEPFFKQN	4	IYQYMDLLVGSDEIG	1	HRTKIEELRQHLRLRWGLTTPDKKHQK	0	EPFLLMMGITL

FIG. 4

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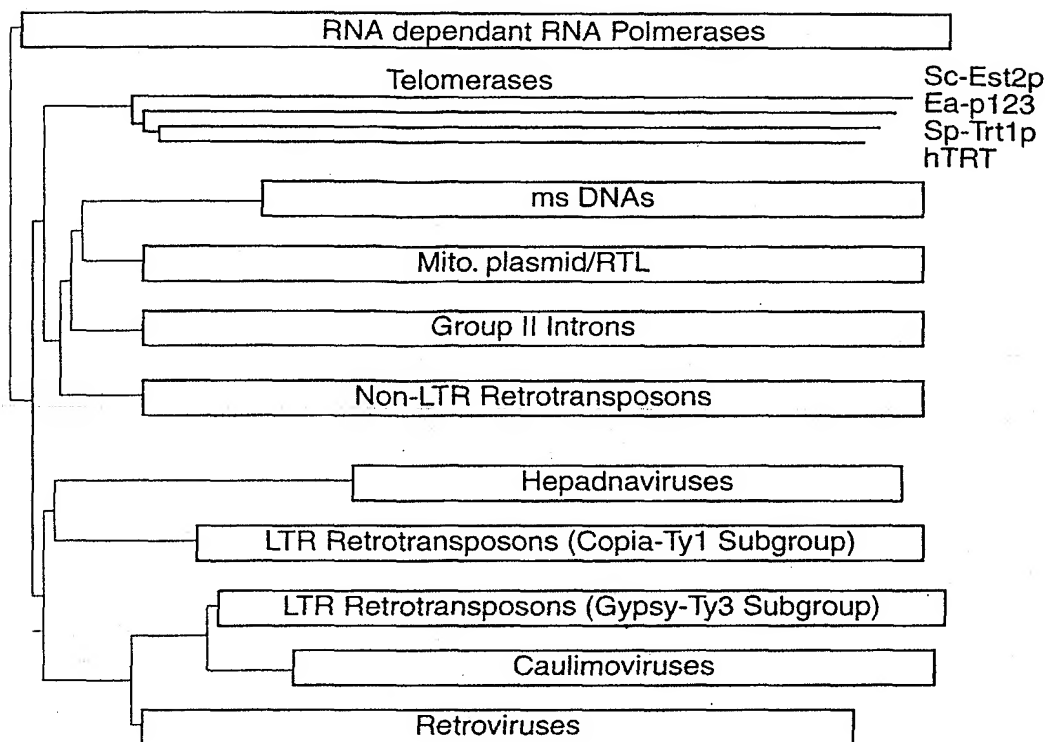


FIG. 6

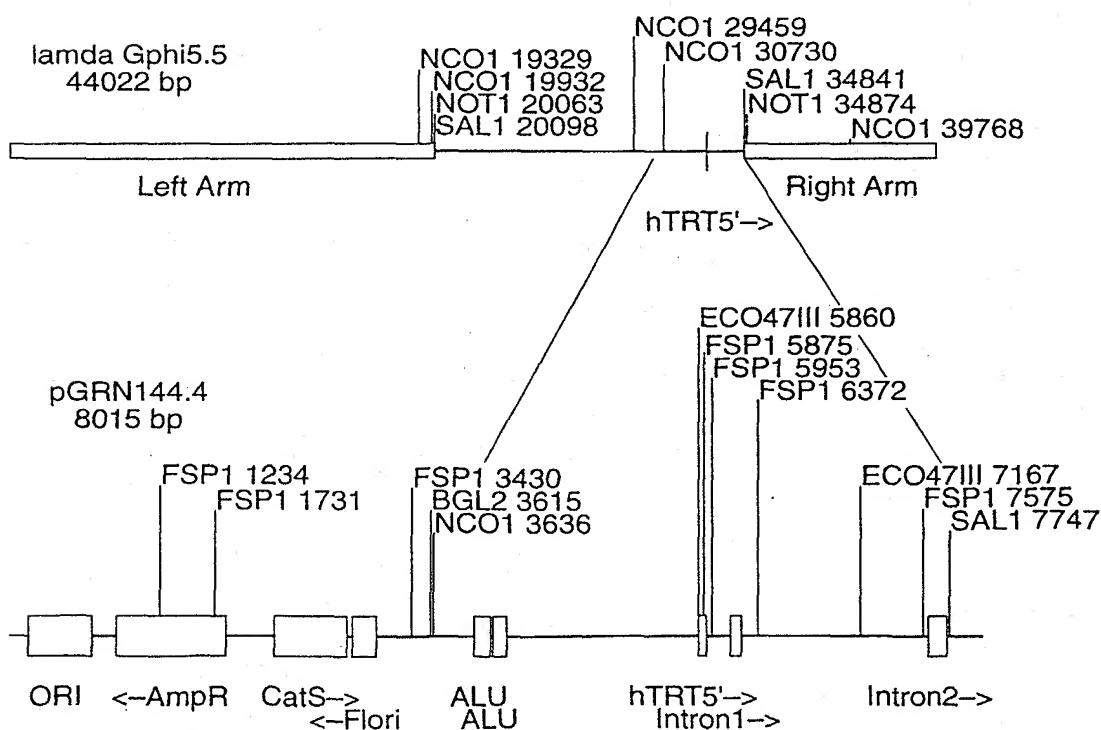


FIG. 7

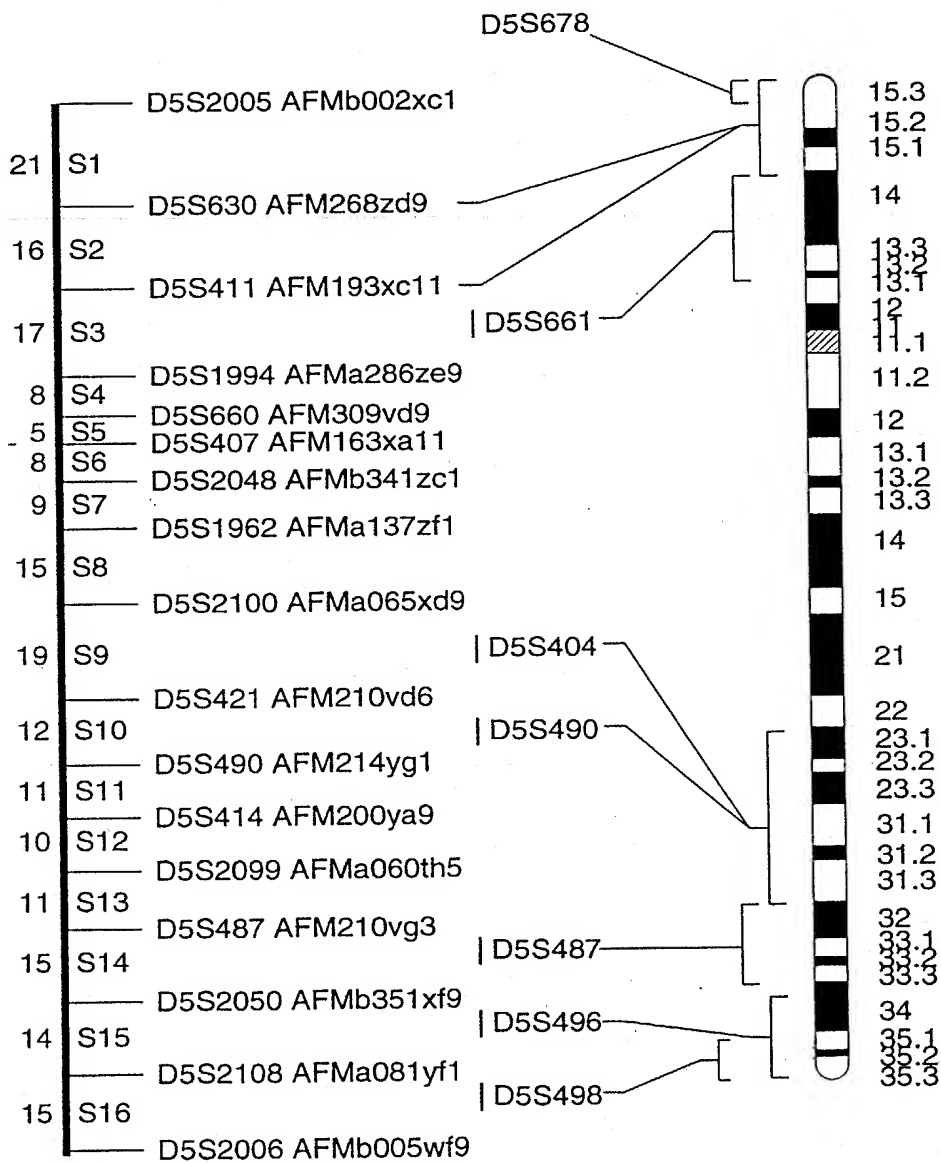


FIG. 8

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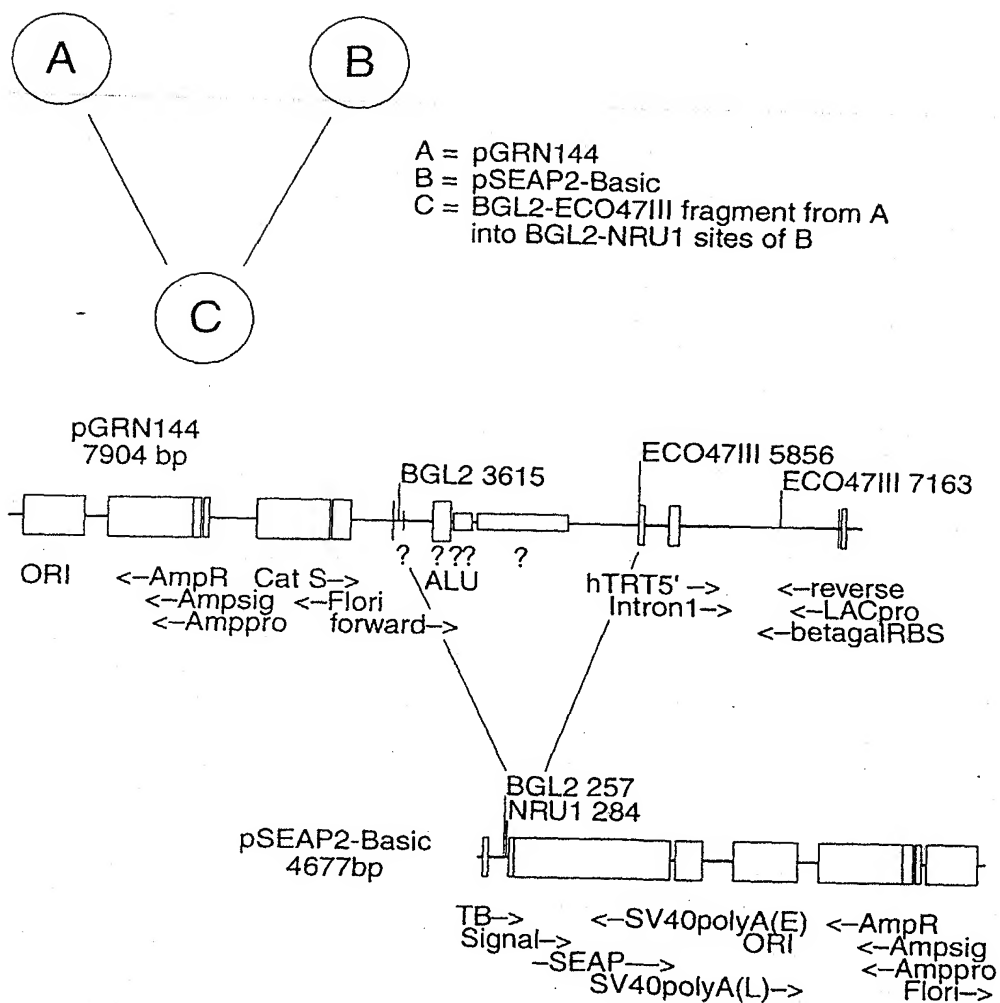


FIG. 9

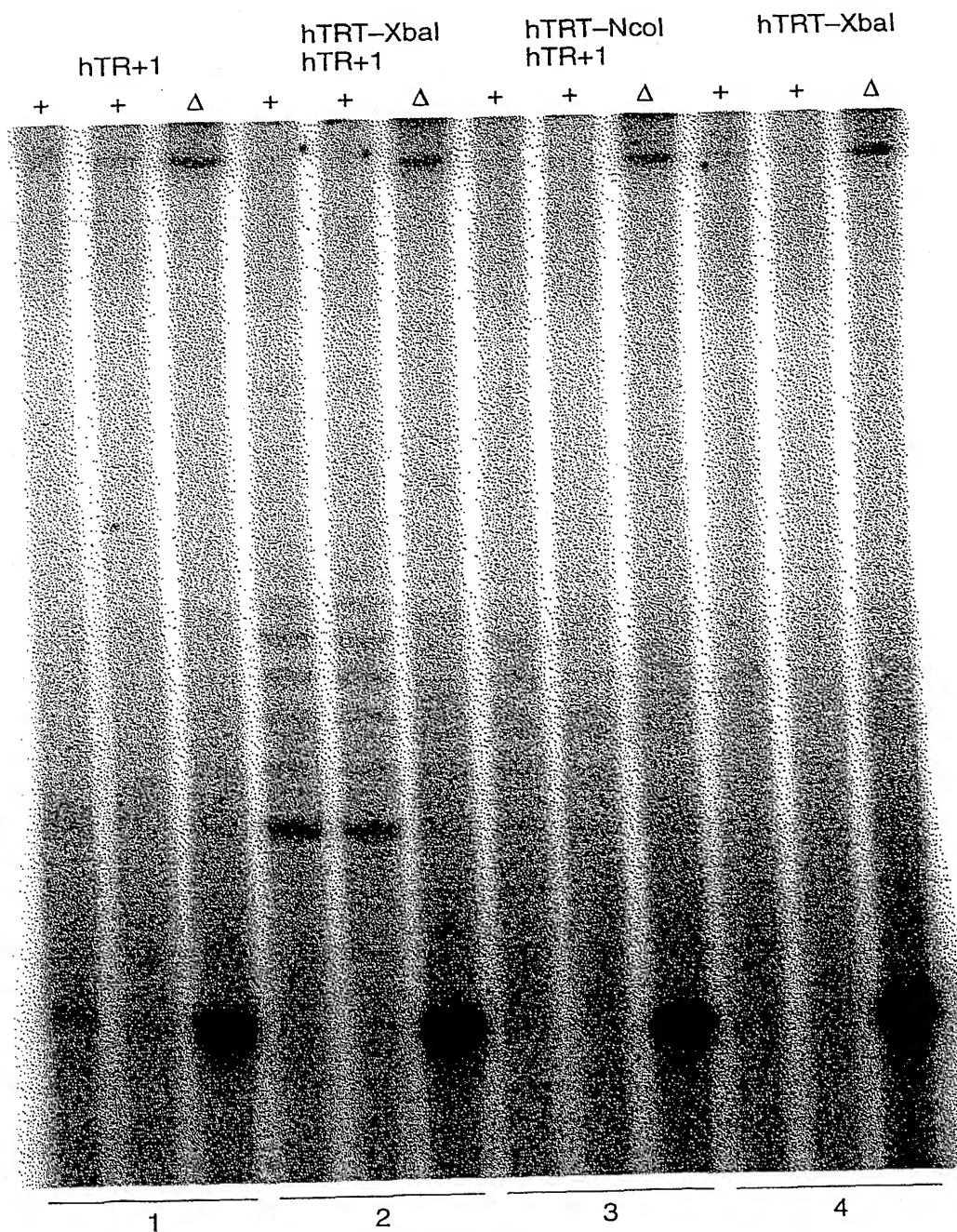


FIG. 10A

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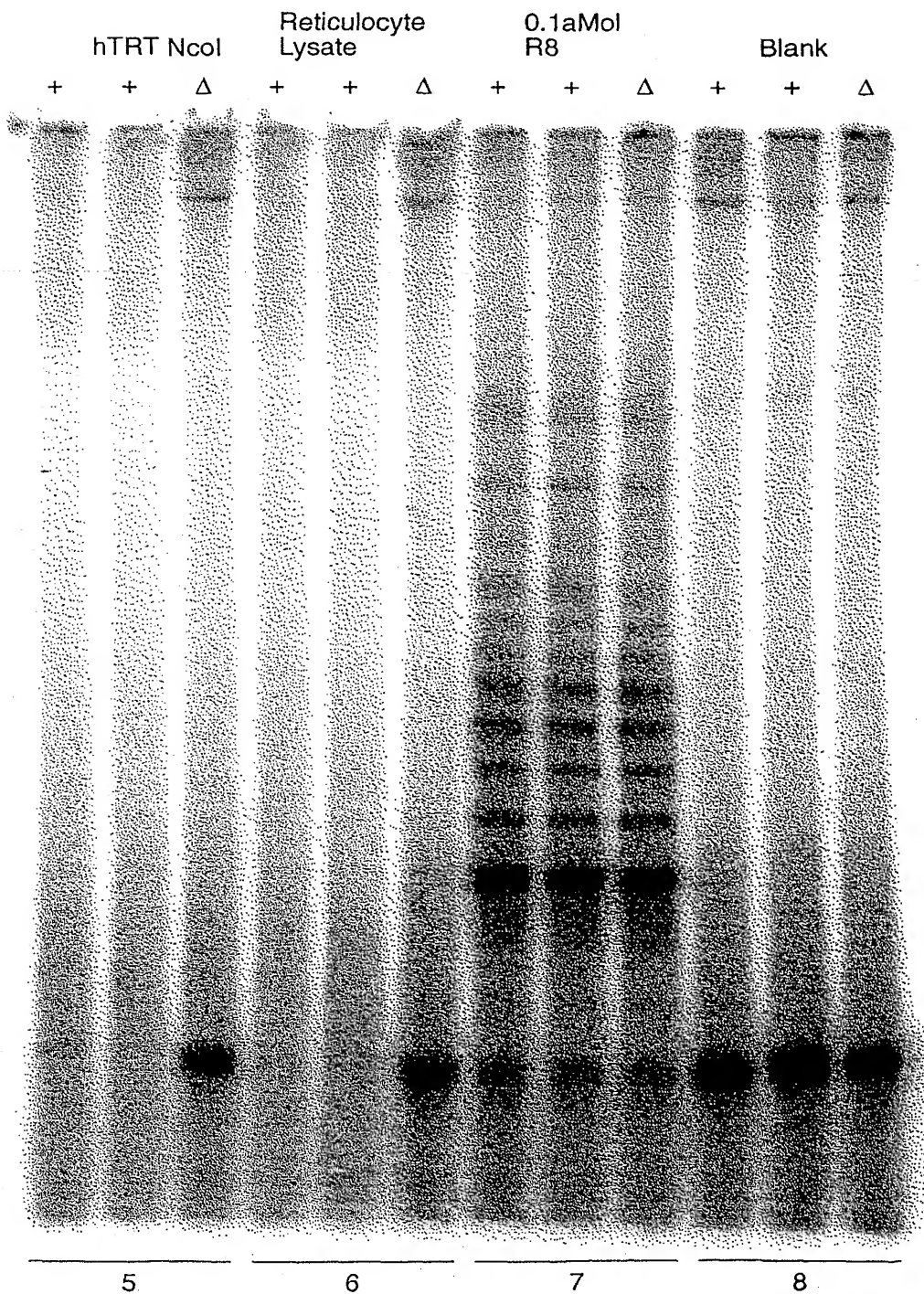


FIG. 10B

Telomerase Specific Motifs

TRT con	MOTIF T	MOTIF T'
hTRT	W1	Y Rk W 1 I E V
spTRT	546 WLMSVYVVELLSFFVYVTTETTFQKNRLFYRKSVWSKLQSIGI 13 EAEVR	
Ea_p123	429 WLYNSFIPILOSPFFVITESSDLNRNRTVYFRKDIWKLRCRPF 12 ENNVR	
Sc_Est2	441 WIFEDLVSLIRCFYVTEQQKSYKTYRKNIDVIMKMSI 12 EKEVE	
	366 WLFRLIPKIIQTFYCTEISSTVT.IVYFRHDTWKLITPFI 9 ENNVC	

Telomerase RT Motifs (Fingers)

TRT con	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
hTRT	R ipkk	fr I	p lyF D cyd i	Y q GipQGs lS l Y
spTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI 104 YVQCQGIPOGGSILSTLLCSLCY		
Ea_p123	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI 99 YLQKVGIPQGSILSSFLCHFYM		
Sc_Est2	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV 117 YKQTKGIPQGLCVSSILSSFY		
RT con	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI 85 YIREDGLFQGSLSAPIVDLVY	hpQG pp hh h	
	p hh h K	hR h	h hDh AF h GY	

Telomerase RT Motifs (Palm, Primer Grip)

TRT con	MOTIF C	MOTIF D	MOTIF E
hTRT	lllrl Ddfl it	g n K	w g s l
spTRT	15 LLLRLVDDFLVIT 15 GVPEYGCVVNLKRTTV 24 WCGLLLDTRTL 192		
Ea_p123	16 VLLRVVDDFLFIT 15 GFEKHNFSTSLKTVI 22 FFGFSVNMRS 176		
Sc_Est2	24 LLMRLTDDYLLIT 15 VSRENGFKFNKKLQT 28 WIGISIDMKTL 174		
RT con	18 LILKLADDFLIIS 15 GFQKYNANAKNRDKILA 25 WKHSSTMNHF 141	Gh h ck h hLG h	
	h y DDhhh F		

FIG. 11

181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGCCCTGGGACGC
CCTGGGCGCGCCGAAAGGCGCGCGACCAACGGGTCACGGACCACACGCACGGGACCCTGCG

NFkB_CS1
GGGRQTYYYQC
NFkB-MHC-I.2
TGGGCTTCCCC

241 ACGGCCGCCCCCGCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG
TGCCGGCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC
CGACCCCAACTCCCGCCGCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB_CS1
GGGRQTYYYQC
NFkB_CS2
RGGGRMTYYCC

Topo_II_cleavage_site
RNYNNCNNGYNGKTNYNY

*****>

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG
TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACGGGCTCACGACGTCTCC

FIG. 12

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAACTTCT GAAGGAAGCTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACCTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACCTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC
1301 AAAAAGTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAC CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGAATC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACC AAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAA ACTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTT TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACCTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTGATC ATTTTATTAT
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

FIG. 13

2401 CCCTGAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
 2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAACTT
 2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAACTACA
 2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAATAC GGAATGGATA
 2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
 2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
 2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
 2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
 2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACCTCT
 2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
 2901 AATACAAGGA CCACTTTAAG AAGAAGTTAG CTATGAGCAG TATGATCGAC
 2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
 3001 CCTTGTTGTC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
 3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
 3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
 3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
 3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT TCTTATATAC
 3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIG. 13
 (CONTINUED)

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCGFQOLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGA
 201 ADMNEPRCCS TCKYNVKNK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
 251 NQFFPKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYEEELFS
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
 401 KNLLLEKINT REISWMQVET SAKHFYFDH ENIYVLWKL RWIFEDLVVS
 451 LIRCFYVTE QQKSYSKTY YRKNIWVIM KMSIADLKKE TLAEVQEKEV
 501 BEWKKS LGFA PGKLRLIPK TFRPIMTFN KKIVNSDRKT TKLTNTNKL
 551 NSHMLKTLK NRMFKDPFGF AVFNYYDDVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ
 701 RNYFKDNL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851 SIDMKTLALM PNINLRIEGL LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
 951 LEVSKIIYSV TRAFFKYLCV NIKDTIFGEE HYPDFFLSTL KHFIIEIFSTK
 1001 KYIFNRVCM LKAKEAKLKS DQCQSLIQYD A

FIG. 14

237 TTG 26344007

1 ggtaccgatttacttcttctcctaagaactgcttccctcgaacgctcctaaatctctggaataatttttacaaga 80
 81 actcaataacaataccaagtccaattccaatatgaaggtgttattagtgatcgataataattttctattttatcggtgtta 160
 161 ccaagtataaggacaaaagaacacttctccctcccaagaacttttacttatttaattttacttttcaaatatttcg 240
 241 ggctcgttactttttaaactggtgactgttttagctgacttcttagccaaacgcgcgttttcccccgcctcattggatat 320
 321 agctctggagtagtgcacagaaaactcttacaatacttctgatgagactatttgatttccacagtcgcgtgcataatc 400
 401 ttaacatggagccttacacttttagatgagtcacgtcgatgatggagtatttggtatcatccaacgttttgcccttgaaga 480
 481 gttgataattatttgcaaatcatgctccttagtgggtgaatccgcgaagttttttagctgctgcacacgtctagcatg 560
 561 attgagatatccaataattttctaccactacaactcctttaacgcggttttatttttctattttctcattctcatgtt 640
 641 ccaaatatgatcatcgtattaggttttttccgttttactcctggaatcgtaaccttttccactattcccccaatga 720
 721 ataactaaattagtttcgtctataattgatagtagaagattggtgattctactcgtgtaattgtattgttttaa 800
 801 gatactttgcaaaacattttattagctatcattataaaaaaaactataataataataatcaatatttgcggtc 880
 881 actatttttaaaacgtttatgatcagtaggacactttgcatatatatagttatgcttaagtgttacttgttaacttgc 958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
 1 M T E H H T P K S R I L R F L E N Q Y V 20

 1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
 21 Y L C T L N D Y V Q L V L R G S P A S S 40

 1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
 41 Y S N I C E R L R S D V Q T S F S I F L 60

 1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
 61 H S T V V G F D S K P D E G V Q F S S P 80

 1199 AAA TGC TCA CAG TCA GAG gtatatatatattttgtttgtattttttctatttcgggatagctaatatatatgggcag 1272
 81 K C S Q S E 86

 1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332
 87 L I A N V V K Q M F D E S F E R R N L 106

 1333 CTG ATG AAA GGG TTT TCC ATG gtaagggtatttctaattgtgaaatattttacacctgcaattactgtttcagaagaga 1405
 107 L M K G F S M 113

 1406 ttgtattttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469
 114 N H E D F R A M H V N G V Q N 128

FIG. 15

353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D L V S T F P N Y L I S I L E S K N W Q 148
 1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacagactgacaagtatag T ATC GGC 1601
 149 L L L E I I G 155
 1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S D A M H Y L L S K G S I F E A L P N D 175
 1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N Y L Q I S G I P L F K N N V F E T V 195
 1722 TCA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
 196 S K K R K R T I E T S I T Q N K S A R K 215
 1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E V S W N S I S I S R F S I F Y R S S Y 235
 1842 AAG AAG TTT AAG CAA G gtaactaataactgttattccttataactaataatttag AT CTA TAT TTT AAC 1907
 236 K K F K Q D L Y F N 245
 1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L H S I C D R N T V H M W L Q W I F P R 265
 1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
 266 Q F G L I N A F Q V K Q L H K V I P L V 285
 2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S Q S T V V P K R L L K V Y P L I E Q T 305
 2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A K R L H R I S L S K V Y N H Y C P Y I 325
 2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D T H D E K I L S Y S L K P N Q V F A 345
 2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
 346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 15

(CONTINUED)

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2268 TTT GAG ATA ATA TTA AAA G gatttgataaaatttaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F E I I L K D L E T 375
 2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
 376 F L K L S R Y E S F S L H Y L M S N I K 395
 2397 gtaatatgccaaattttttaccatttaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
 396 I S E I E W L V L G 405
 2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
 406 K R S N A K M C L S D F E K R Q I F A 425
 2526 GAA TTC ATC TAC TGG CTA TAC GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2585
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445
 2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
 446 I T E S S D L R N R T V Y F R K D I W K 465
 2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705
 466 L L C R P F I T S M K M E A F E K I N E 485
 2706 gatttttaagatatttttgcaaaagctaattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486 N N V R M D T Q K T 495
 2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
 496 T L P P A V I R L L P K K N T F R L I T 515
 2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcactcaatgtactttacttctaatctatta 2906
 516 N L R K R F L I K 524
 2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 525 M G S N K K M L V S T N Q T L R P V 542
 2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
 543 A S I L K H L I N E S S G I P F N L E 562
 3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 15

(CONTINUED)

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CGTTTTCAGGTTTC

3089 tataataatgcgcgattcctcattatttaatttcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155
582 R K K Y F V R I D I 591
3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CQG ATT GTT AAA AAG AAA CTC 3215
592 K S C Y D R I K Q D L M F R I V K K L 611
3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275
612 K D P E F V I R K Y A T I H A T S D R A 631
3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttttttttttttttttttttttaacaa 3343
632 T K N F V S E A F S Y F 643
3344 attcttttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
644 D M V P F E K V V Q L L S M K T 659
3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465
660 S D T L F V D F V D Y W T K S S E I F 679
3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgtgaattgttaataca 3532
680 K M L K E H L S G H I V K 692
3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693 I G N S Q Y L Q K V G I P Q G S 708
3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709 I L S S F L C H F Y M E D L I D E Y L S 728
3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729 F T K K K G S V L L R V V D D F L F I T 748
3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
749 V N K K D A K K F L N L S L R G 764
3778 taagtcttaaccgtttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765 F E K H N F S T S L E K T V 778
3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
779 I N F E N S N G I I N N T F F N E S K K 798

FIG. 15
(CONTINUED)

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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R M P F F G F S V N M R S L D T L L A C 818
3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P K I D E A L F N S T S V E L T K H M G 838
4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839 K S F F Y K I L R S 848
4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S L A S F A Q V F I D I T H N S K F N S 868
4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C C N I Y R L G Y S M C M R A Q A Y L K 888
4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889 R M K D I F I P Q R M F I T D 903
4275 aaagtcattaattaaccccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904 L L N V I G R K I W K K L A 917
4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E I L G Y T S R R F L S S A E V K W 935
4402 ggtctcgagacttcagcaataattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936 L F C L G M R D G L K 946
4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966
4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA ATA 4588
967 D L I K P L R P V L R Q V L F L H R R I 986
4589 GCT GAT TAA tgcatttttcaatttattatatatacatccttttattactggtgtctttaacaataattattactaagtata 4665
987 A D * 989

FIG. 15
(CONTINUED)

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4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaataatctcgttattagttttgattgacttgctct 4745
4746 ttatccttataacttttaagaaagattgacagtggttgcctgactactgcccacatgcccattaaacgggagtggttaaca 4825
4826 ttataagtaatacatgaggtaaatctcctttcaattagaataaggaaagtgggtttctataatgaataatgcccgaacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaaggggattaaagcatatccgaaggaagagagtaatataccagtggtt 4985
4986 gttgaagaaagcaaggaataatttggaacaagcttctgcagatgacaggtctaaattttggtgaccgaattttggttaaaagc 5065
5066 cccagggtatccatggtggccgaccttgctactgagacgaaagaaactaaggatagtttgaataactaataagctcaattta 5145
5146 atgtccttataaaggttttttccctgacttcaattttgcatgggtgaaagaaataagtggttaagccattattggat 5225
5226 tcgaaatagccaaattcttgggttcctcaagcgggaagtctaaagaaacttatgaagcttatgaggctcaaaaactcc 5305
5306 tccatgattaaaggaggaatcttccaccgatagggaatggatagcttaccagctgctgaggagaagccataatttttgc 5385
5386 aaaaaagaaaatatcatctgggagacatctcttgatgaatcagatcgaggagagtatctccaggggatccttgatgtcaata 5465
5466 acttctatttctgaaatgatggctcctactgtcgcttcgacttctcgtagctctacgcaggttaagtgaacaaagggtacc 5544

FIG. 15
(CONTINUED)

ATTORNEY

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1 gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcatgccc
61 gcgcgctccc cgctgcccag ccgtgctgct cctgctgctc agccactacc ggcaggtgct
121 gccgctggcc acgttctgtc ggcgcctggg gccccagggc tggcggtggg tgcagcgctg
181 ggacccggcg gctttccgcg cgctgggtgg ccagtgcctg gtgtgctgct cctgggacgc
241 acggccgccc ccgcgcgccc cctccttccg ccaggtgtcc tgctgaagg agctgggtgg
301 ccgagtgtct cagaggctgt gcgagcgctg ccggaagaac gtgctggcct tcggcttcgc
361 gctgctggac gggggcccgcg gggggccccc cgaggccttc accaccagcg tgcgcagcta
421 cctgccccaa acgggtgacc acgcactcgc ggggagcggg gcgtgggggc tgctgctgct
481 ccgcgtggcg gacgacgtgc tggttcacct ctgggcacgc tggcgctct ttgtgctggt
541 ggctcccagc tgcgcctacc aggtgtgctg gccgcgctg taccagctcg gcgctgccac
601 tcaggcccgg cccccgccac acgtagtggg accccgaagg cgtctgggat gcgaacgggc
661 ctggaaccat agcgtcaggg aggcgggggt cccccgggc ctgccagccc cgggtgcgag
721 gagcgcgggg ggcagtggca gccgaagtct gccgttgccc aagaggccca ggcgtggcgc
781 tgcccctgag ccggagcggg cgcctgttgg gcagggttcc tggggccacc cgggcaggac
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagacccg ccgaagaagc
901 cacctctttg gagggtgcgc tctctggcac gcgcactcc caccatccg tgggcccgca
961 gcaccacgcg gggcccccac ccacatcgcg gccaccacgt cctggggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttctc ctactcctca ggcgacaagg agcagctgct
1081 gccctccttc ctactcagct ctctgagggc cagcctgact ggcgctcgga ggcctgtgga
1141 gaccatcttt ctgggttcca ggcctgggat gccagggact ccccgaggt tggcccgcct
1201 gccccagcgc tactggcaaa tgcggccctt gtttctggag ctgcttggga accacgcgca
1261 gtgcccctac ggggtgtctc tcaagacgca ctgcccgtcg cgagtgcgg tcaccccagc
1321 agccgggtgc tgtgcccggg agaagcccca gggctctgtg gcggcccccg agggaggaga
1381 cacagacccc cgtgcctgg ctgcagctgt ccgcagcac agcagccct ggcaggtgta
1441 cggcttctgt cgggcctgct tgcgcggctt ggtgccccca ggctcttggg gctccaggca
1501 caacgaacgc cgttctctca ggaacaccaa gaagtctatc tccctgggga agcatgccaa
1561 gctctcgtgc caggagctga cgtggaagat gacgctgcgg gactgcctt ggtgcgcag
1621 gagcccaggg gttggctgtg ttccggcgcg agagcacctg ctgctgagg agatcctggc
1681 caagtctctg cactggctga tgagtgtgta cgtcgtcgag ctgctcagg ctttctttta
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
1801 caagtatgca agcattggaa tcagacgca ctgaagagg gtgcagctgc ggcagctgtc
1861 ggaagcagag gtcaggcagc atcgggaagc caggcccgcc ctgctgacgt ccagactccg
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tgcgtgggagc
1981 cagaacgttc cgcagagaaa agaggggcga gcgtctcacc tcgagggtga aggcactgtt
2041 cagcgtgctc aactacgagc gggcgcgcg ccccgccctc ctgggcgct ctgtgctggg
2101 cctggacgat atccacaggg cctggcgcac ctctgtgctg cgtgtgcggg cccaggaccc
2161 gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccc
2221 ggacaggctc acggaggtea tcgcagcat catcaaacc cagaacacgt actgcgtgcg
2281 tcggtatgct gtcgtccaga aggcgcgcca tgggcacgtc cgcaaggcct gggagtgcca
2341 cgtctctacc ttgacagacc tccagccgta catgcgacag ttcgtggctc acctgcagga
2401 gaccagcccg ctgagggtat ccgtgctcat cgagcagagc tctcctctga atgaggccag
2461 cagtggcctc ttgcagctct tctcagctt catgtgccac cagcccgctg gcactagggg
2521 caagtctac gtccagtgcc aggggatccc caggggctcc atcctctcca cgtgctctg
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct
2641 gctcctgctg ttggtgggat atttcttgtt ggtgacacct cactcacc cgcgaaaaac
2701 cttcctcagg accctggctc gagggtctcc tgagtatggc tgcgtgggta acttgcgga
2761 gacagtgggt aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat
2821 gccggcccac ggctattcc cctggtgcgg cctgctgctg gatacccgga cctggagggt
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca ccttcaaccg
2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggtgaagtg
3001 tcacagcctg tttctggatt tgcagggtga cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacaggtt tcaogcatgt gtgctgcagc tcccatttca
3121 tcagcaagtt tggagaacac ccacatttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcccgcg
3241 cggccctctg cctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctggggtoa ctcaggacag cccagacgca
3361 gctgagtcgg aagctccccg ggaacagcgt gactgcctg gaggcccgag ccaaccggc
3421 actgccctca gacttcaaga ccatcctgga ctgatggoca cccgccaca cccagccgga
3481 gagcagacac cagcagccct gtcacgcgg gctctacgtc ccagggaggg aggggaggcc
3541 cacaccaggg cccgcaccgc tgggagctct aggcctgagt gagtgtttgg ccgaggcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaagggtc
3661 gagtgtccag cacacctgcc gtcttcaact cccacaggc tggcgctcgg cctccacca
3721 gggccagctt ttctcacca ggagcccgcc ttccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac cctcgcctt gccctccttt gccttccacc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgc caaaggtgtg
3901 cctgtacac ccgtgacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

FIG. 16

MPRAPRCRAVRSLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
AAFRALVAQCLVCPWDARPPPAAPSFRQVSLKELVARVLQRL
CERGAKNVLAFGFALLDGARGGPPPEAFTTSVRSYLPNTVTDALR
GSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLY
QLGAATQARPPPHASGPRRRLGCERAWNHVSREAGVPLGLPAPG
ARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
PSDRGFCVVSAPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPP
STSRPPRPWDTPCPPVYAETKHFVLYSSGDKEQLRPSFLLSSLRP
SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL
LGNHAQCYPYGVLLKTHCPLRAAVTPAAGVCAREKPOGSVAAPPEE
EDTDPRRLVQLLRQHSSPWQVYGFVRACLRLRLVPPGLWGSRHNE
RRFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVGC
VPAAEHRLREEILAKFLHWMLSVYVVELLRSFFVYTETTFQKNR
LFFYRKSWSKLQSIGIRQHLKRVQLRELSEAENVQHREARPAL
LTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA
LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPP
ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQ
KAAHGHRVRAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVI
EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSI
LSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA
KTFLRTLVRGVPEYGCVVNLKRTVVNF PVEDEALGGTAFVQMPA
HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR
NMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRF
HACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL
GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTVVPLLGSLRTAQ
TQLSRKLPGTTLTALEAAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
TTATGTACACGAGACCACGTTTCAAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT
GTCGGAAGCAGAGGTACAGCAGCATCGGGAAGCCAGGCCCCGCCCTGCTGACGTCCAGACT
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGG
AGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAT
GTTACAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT
GGGCTTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGA
CCCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
CCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT
GCGTCGGTATGCGGTGGTCCAGAGGCCGCCCATGGGCGACGTCCGCAAGGCCCTCAAGAG
CCACGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCT
GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGC
TGCTCCTGCGCTTTGGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGCGAAAA
CCTTCTCAGGACCTTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGGGA
AGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGA
TGCCGGCCCCACGGCCTATTCCCTTGGTGGCGCTGCTGCTGGATACCCGGACCTGGAGG
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGT
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTC
ATCAGCAAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTCTGACACGGCCTCCC
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTGCTGGGGGCCAAGGGCGCCG
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTAAGC
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCGCAGCCAACCCGG
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG
AGAGCAGACACAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGGCGG
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTGTTGGCCGAGGCCT
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
AGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC
CCAGATTGCGCCATTGTTACCCCTCGCCCTGCTTCCCTTTCCTTCCACCCACCACATC
CAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGACCAAAGGTGT
GCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTG0AAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIG. 18

MetSerValTyrValValGluLeuLeuArgSerPhePhe
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe
PheTyrArgLysSerValTrpSerLysLeuGlnSerIle
GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu
LeuSerGluAlaGluValArgGlnHisArgGluAlaArg
ProAlaLeuLeuThrSerArgLeuArgPheIleProLys
ProAspGlyLeuArgProIleValAsnMetAspTyrVal
ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu
ArgLeuThrSerArgValLysAlaLeuPheSerValLeu
AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla
SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg
ThrPheValLeuArgValArgAlaGlnAspProProPro
GluLeuTyrPheValLysValAspValThrGlyAlaTyr
AspThrIleProGlnAspArgLeuThrGluValIleAla
SerIleIleLysProGlnAsnThrTyrCysValArgArg
TyrAlaValValGlnLysAlaAlaHisGlyHisValArg
LysAlaPheLysSerHisValLeuArgProValProGly
AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln
ProValLeuArgArgHisGlyGluGlnAlaValCysGly
AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG
1
met
10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC
20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG
30
40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT
50
60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC
70
80
90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC
100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG
110
120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

FIG. 20

```

                                130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

                                140
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

                                170
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                180
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

                                190
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                210
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

                                220
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                230
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

                                240
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                250
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

                                260
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                270
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

                                280
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                290
                                300
                                310
                                320
                                330

```

FIG. 20
(CONTINUED)

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

360
370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

390
400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

420
430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

450
460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

480
490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

510
520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

540

FIG. 20
(CONTINUED)

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

FIG. 20
(CONTINUED)

1004452-04402

750
his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770
val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

790
gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800
ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTTGGT

807
GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA
GTATGGCTGCGTGGTGAACCTGCGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGC
CCTGGGTGGCAGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT
GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAA
ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTGTCAGGTGAACAG
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCT
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG
GATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT
GTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT
GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC
TGCCCTGGAGGCCGACGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG
ATGGCCACCCGCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGGCT
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG
CCTGAGTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG
GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC
CACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC
CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTTCAACCCCTCGCCCTGCC
CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC
TGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT
GGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG
AGTTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20
(CONTINUED)

FIG. 21

4321 GGTGTTTTTAAGCCAATNANAAAATTTTTTATGTTGTTNNNNNNNNNNNNNNNNNNNN
CCACAAAAATTCGGTTANTNTTTTAAAAAANTACAACAAANNNNNNNNNNNNNNNNNNNN
4381 NNN
NN
4441 NNN
NN
4501 NNN
NN
4561 NNN
NN
4621 NNN
NN
4681 NNN
NN
4741 NNN
NN
4801 NNN
NN
4861 NNN
NN
4921 NNN
NN
4981 NNN
NNCCGGTGNNNGAGGG
NNNGGCCACNNNCTCCC
5041 NGCCANGRAGGGGGCCAGGTTCCAANTTCCAACCKTTTWTGGARGGACNGCCCCCAGGG
NCGGTNCYTCCCCCGGTCCAAGGTTNAAGGGTTGGMAAAAWCCTYCCTGNCGGGGGTCCC
5101 GGGGATRAACAGANTNGGGGGKGGTWWGGTTNAKGGTGGGAACNCCTTNGCGCCTGGAG
CCCCATAYTTGTCTNANCCCCMCCAWCCAANTMCCACCCTTGNGGAANCGSCGGACCTC
5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGCGGGGRAGTTG
TTGCACGTTTCTCCTTTACTTCCCGGACMCAGTTCCCTCGGGTTCANCCGCCCCYTCAAAC
5221 CAGGGAGGCACTCCGGGGAGGTCCSGCGTGCCCGTCCAAGGGAGCAATGCGTCTCTCGGG
GTCCCTCCGTGAGGCCCTCCAGGSCGCACGGGCAGGTTCCTCGTTACGCAGGAAGCCC
5281 TTCGTCCCCAWGCCGCGTCTACGCGCCTYCCGTCTCTCCCTTCACGTTCCGGCATTCGTG
AAGCAGGGGTWCGGCGCAGATGCGCGGARGGCAGGAGGGGAAGTGCAAGGCCGTAAGCAC
5341 GTGCCCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG
CACGGGCCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTGCGGACCCAGAGGCCTAGTC
5401 GCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCAGGGCCTCCACATCATGGCCCCCT
CGGTGCGCGGTTTCCAGCGGCGTGCGTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

FIG. 21
(CONTINUED)

5461 CCCTCGGGTTACCCACAGCCTAGGCCGGATTGACCTCTCTCCGCTGGGGCCCTCGCCT
GGGAGCCCAATGGGGTGTGCGATCCGGCCTAAGCTGGAGAGAGGCGACCCCGGGAGCGGA

Sp1

5521 GGCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCCATACCC
CCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTATGGG

5581 CCGGGTCCGCCCCGAAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTGGATTGCG
GGCCCAGGCGGGCCTTCGTGACGCGACAGCCCCGGTCCGGCCCGAGGGTCACCTAAGCG

Topo_II_cleavage_site

5641 GGGCACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAAGGACTGGGGACCCGGGCACC
CCCGTGTCTGCGGGTCTTGGCGCGAAGGGTGCACCGCCTTCCTGACCCCTGGGCCCCGTGG

E2F

5701 CGTCCTGCCCCCTTACCTTCCAGCTCCGCTTCTTCCGCGCGGACCCGGCCCCGTCCCGAA
GCAGGACGGGGAAGTGAAGGTGAGGCGAAGAAGCGCGCCTGGGCCGGGGCAGGGCTT

E

5761 CCCTTCCCAGGTCCCGGGCCAGCCCCCTCCGGGCCCTCCAGCCCCCTCCCCTTCTTTTC
GGGAAGGGTCCAGGGCCGGGTGCGGGAAGGCCCGGGAGGGTCCGGGAGGGGAAGGAAAAG

Sp1

=====

2F

NFkB

h

5821 CGCGGCCCGCCCTCTCCTTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCTGTGCGCA
GCGCCGGGGCGGGAGAGGAAGCGCCGCGCTCAAAGTCCGTGCGGACGCAGGACGACGCGT

5860

ECO47III

5875

FSP1

TRT5'

*****>

5881 CGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCG
GCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTCGGC

5941 TCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTGCTGCGGC
ACGCGAGGGACGACGCGTCCGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACGCCG

5953

FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGC
CGGACCCCGGGGTCCCGACCGCCGACCACGTGCGCCCCCTGGGCCCGCGAAAGGCGCGCG

6061 TGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCCGCCCTT
ACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGCGGGGGGCGCGGGGGA

NFkB

=====

FIG. 21
(CONTINUED)

```
*****
6121 CCTTCCGCCAGGTGGGCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGG
    GGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGACGGCCGACCCCAACTCCCGCCGGCCCC

                                         Topo_II_cleavage_s
                                         :::::::::::::::
                                         NFkB
                                         =====

Intron1
*****>
6181 GGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTC
    CCTTGGTCGCTGTACGCCTCTCGTTCGCTCCGCTGAGTCCCGCAAGGGGGCGTCCACAG

ite
:

6241 CTGCCTGAAGGAGCTGGTGGCCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAA
    GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCCGCGGGGGCCCCCGAGGCCTT
    GCACGACCGGAAGCCGAAGCGCGACGACCTGCCCCGGGCGCCCCGGGGGGGCTCCGGAA

6361 CACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGG
    GTGGTGGTCGCACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACCCCCCTCGCC
        ^
        6372
        FSP1

6421 GGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACG
    CCGCACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGACGACCGTGC

6481 CTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCT
    GACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCCGGCGGCGA

6541 GTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCGCCACACGCTAGTGACCCCGAAG
    CATGGTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGCTTC

6601 GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGG
    CGCAGACCCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCC
    GGACGGTCGGGGCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGG

6721 CAAGAGGCCCAGGCGTGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTC
    GTTCTCCGGGTCCGCACCGCGACGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAG

6781 CTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACC
    GACCCGGGTGGGCCCCGTCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAGTGG

6841 TGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTC
    ACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAG

6901 CCACCCATCCGTGGGCGGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCACG
    GGTGGGTAGGCACCCGGCGGTCTGTTGGTGCGCCCGGGGGTAGGTGTAGCGCCGGTGGTGC
```

FIG. 21
(CONTINUED)

6961 TCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTC
AGGGACCCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAG
7021 AGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGAC
TCCGCTGTTCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCCGACTG
7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGAC
ACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCCCTG
7141 TCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGA
AGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGACCT

7167
ECO47III

7201 GCTGCTTGGGAACACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCT
CGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGGCGA
7261 GCGAGCTGCGGTACCCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGT
CGCTCGACGCCAGTGGGGTCGTGCGCCACAGACACGGGGCCCTCTTCGGGGTCCCGAGACA
7321 GGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCA
CCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCGAGCGGACCACGTGACGAGGCGGTCTGT
7381 CAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGTCCCC
GTCGTGCGGGACCGTCCACATGCCGAAGCACGCCCCGACGGACGCGGCCGACCACGGGGG
7441 AGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCAT
TCCGGAGACCCCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTA
7501 CTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG
GAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCGACTGCACCTTCTACTCGCACGC

7561 GGA CTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCCAGG
CCTGACGCGAACCGACGCGTCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGGTCC

7575
FSP1

Intron2

7621 CCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCTCCT
GGGGTCTCGACTTACGTTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGAGGA

7681 GTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTGAGTGGACACGGTG
CAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGCCAC

**>

7741 ATCGAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATA
TAGCTCCAGCTGAGATCTCCTAGGGGCCCATGGCTCGAGCTTAAGCATTAGTACCAGTAT

7747
SAL1

FIG. 21
(CONTINUED)

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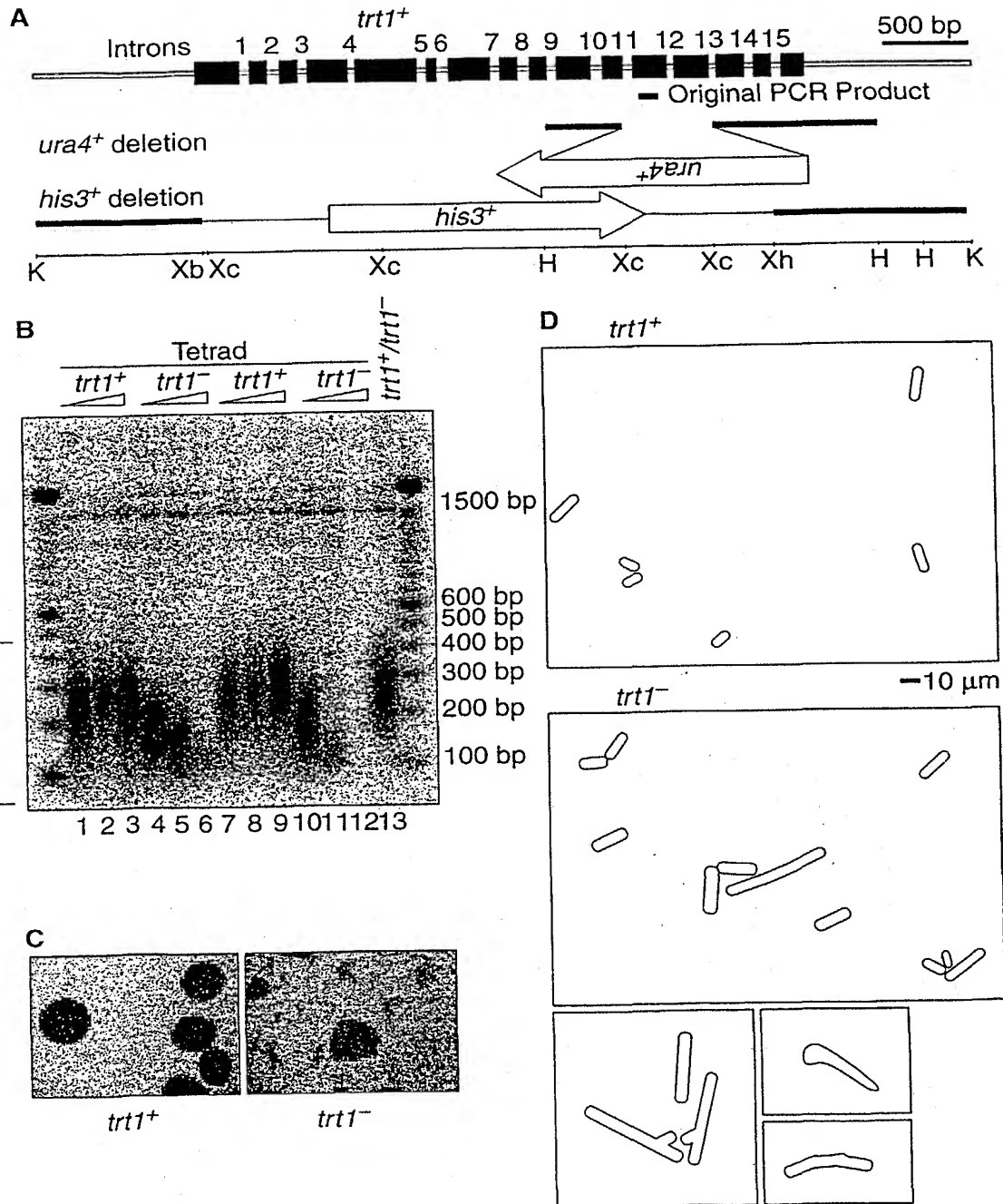


FIG. 22

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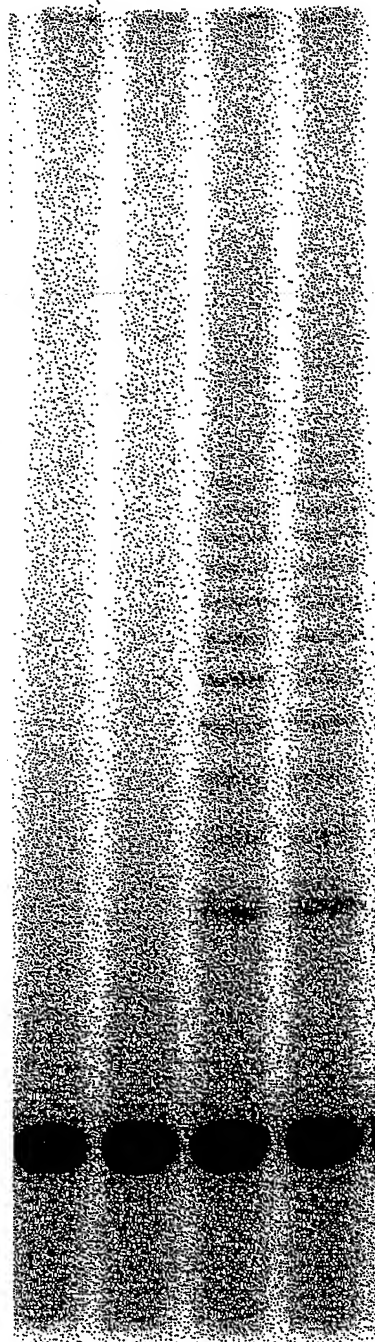
gccaagttcctgcactggctgatgagtgtgtacgtcgctcgagctgctcaggtctttcttt
tatgtcacggagaccacgtttcaaaagaacaggctctttttctaccggaagagtgtctgg
agcaagttgcaaagcattggaatcagacagcacttgaagaggggtgcagctgcgggacgtg
tcggaagcagaggtcaggcagcatcggaagccaggcccgccctgctgacgtccagactc
cgcttcatccccaagcctgacgggctgcggccgattgtgaacatggactacgtcggtggga
gccagaacgttccgcagagaaaaagaggccgagcgtctcacctcgaggggtgaaggcactg
ttcagcgtgctcaactacgagcgggcgcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
ACCAGCCCCGCTGAGGGATGCCGTCGTTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC
AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC
AGGGGCAAGTC

FIG. 24

pBBS212 pGRN133



← Internal Control

Approximate Cell No.	5,000	5,000	5,000	5,000
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FIG. 25